

# Quantitative PCR

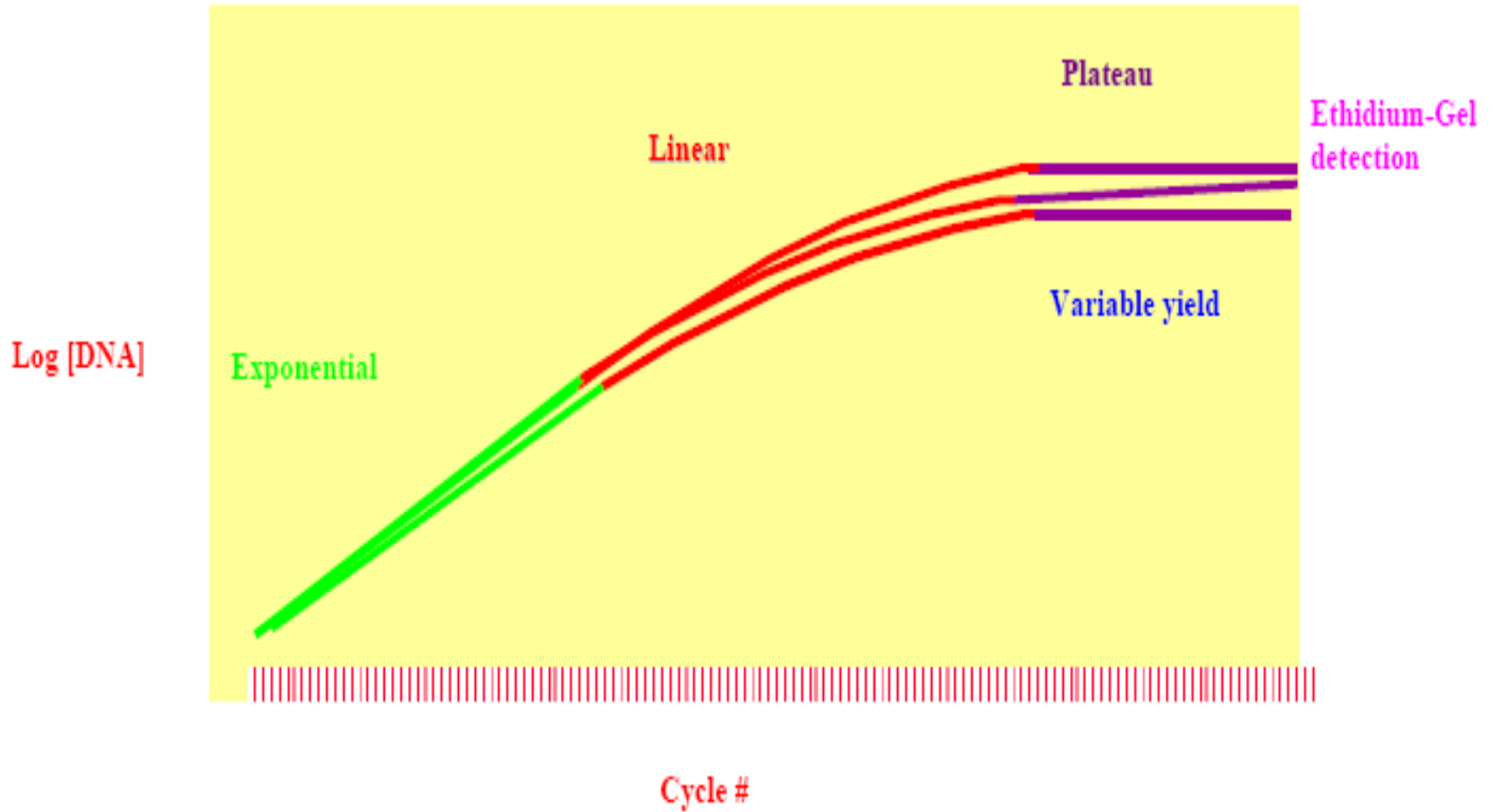
- ▶ END POINT product analysis

**Traditional method that uses Agarose gels for detection of PCR amplification at the final phase or end-point of the PCR reaction**

# A basic PCR run can be broken up into three phases

- ▶ **Exponential:** Exact doubling of product is accumulating at **every cycle** (assuming 100% reaction efficiency). The reaction is very specific and precise.
- ▶ **Linear (High Variability):** The reaction components are being consumed, the reaction is slowing, and products are starting to degrade.
- ▶ **Plateau (End-Point Gel detection for traditional methods):**  
The reaction has stopped, no more products are being made and if left long enough, the PCR products will begin to degrade

# PCR Phases



# Limitations of End-Point PCR

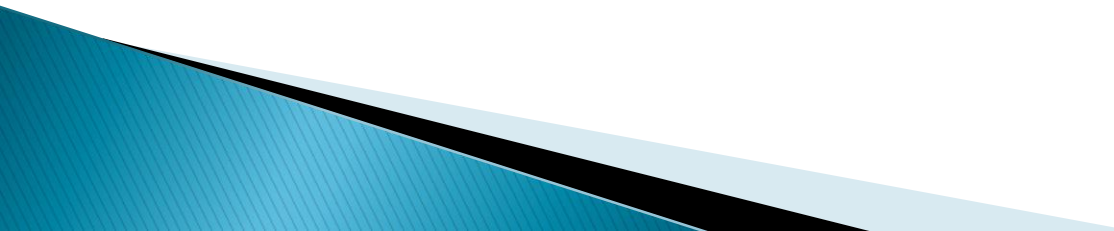
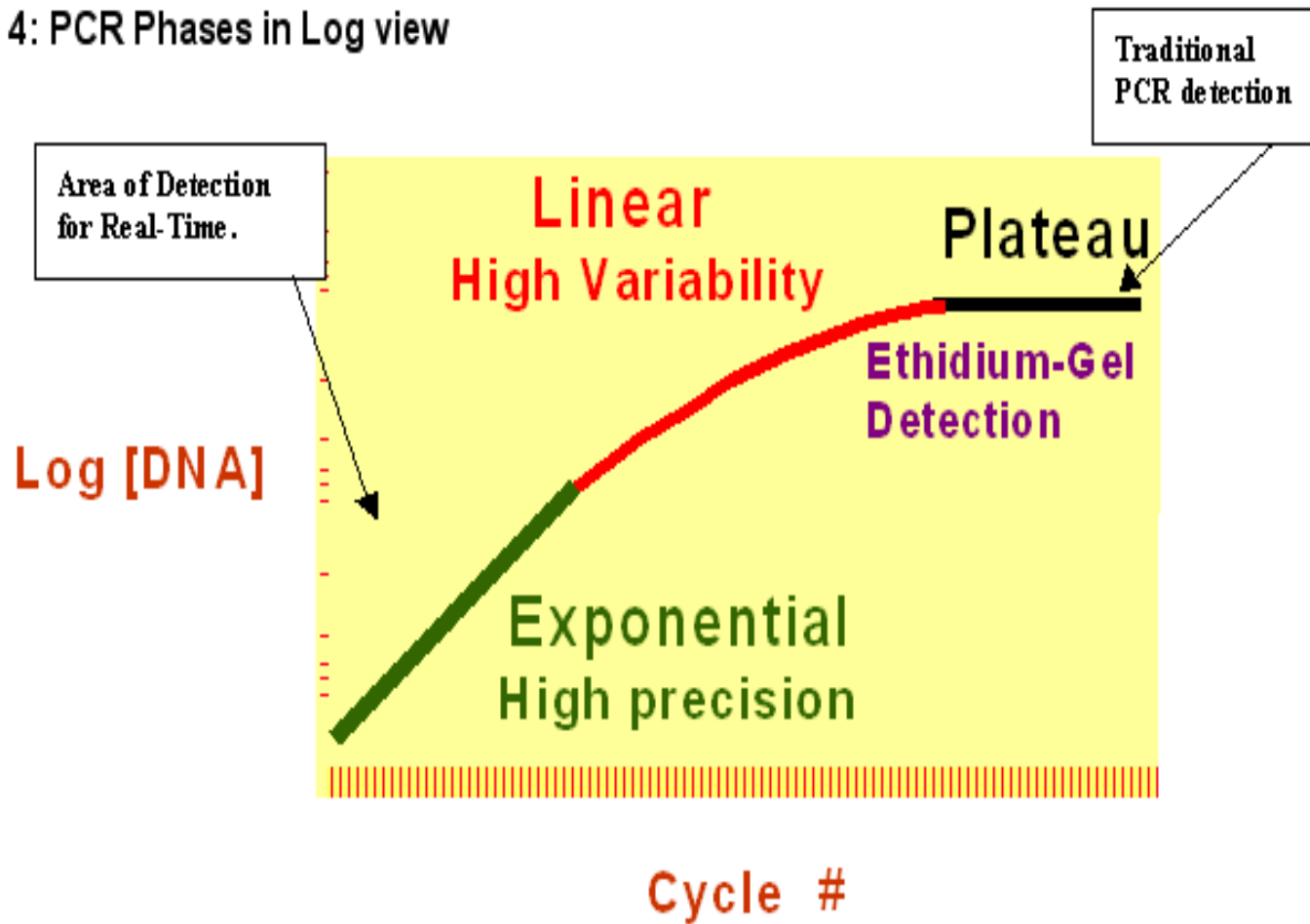
- ▶ Time consuming (Post PCR processing)
  - ▶ Poor Precision (Results are based on size discrimination)
  - ▶ Low sensitivity (The end point is variable from sample to sample. While gels may not be able to resolve these variabilities in yield).
  - ▶ Results are not expressed as numbers
  - ▶ Non - Automated
- 

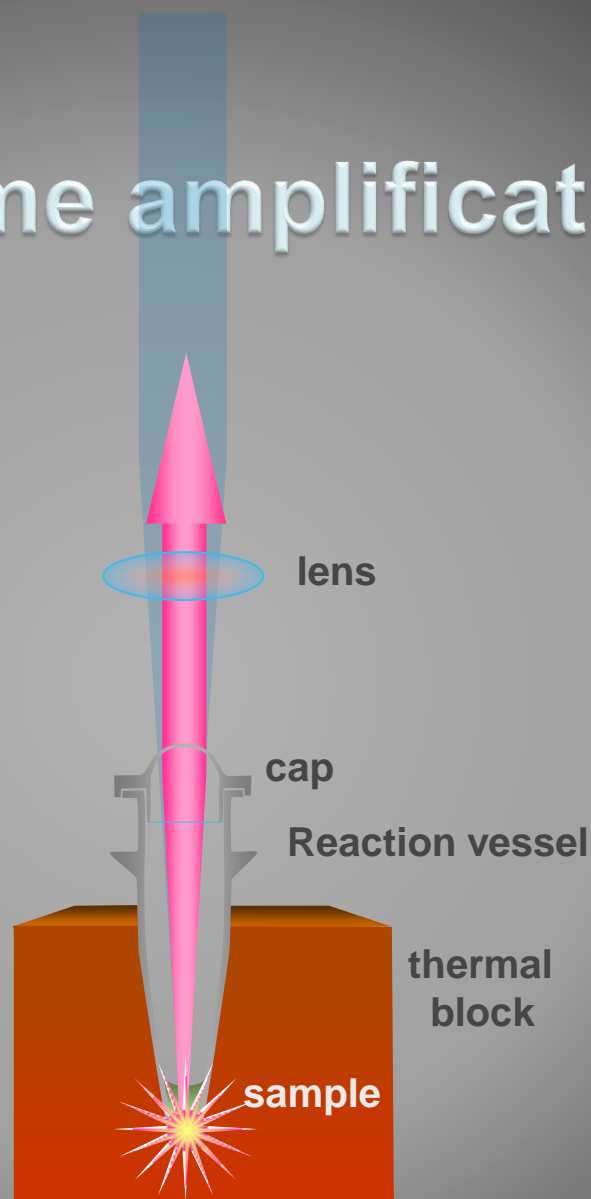
Figure 4: PCR Phases in Log view



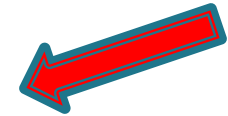
# The Evolution of PCR to Real-Time

- ▶ From detection at the **end-point** of the reaction to detection **while the reaction is occurring**

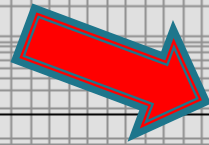
# What is real-time amplification?



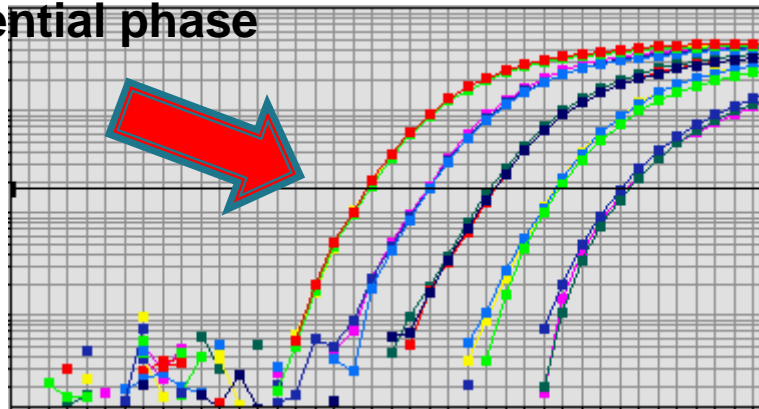
**Plateau effect**



**Exponential phase**

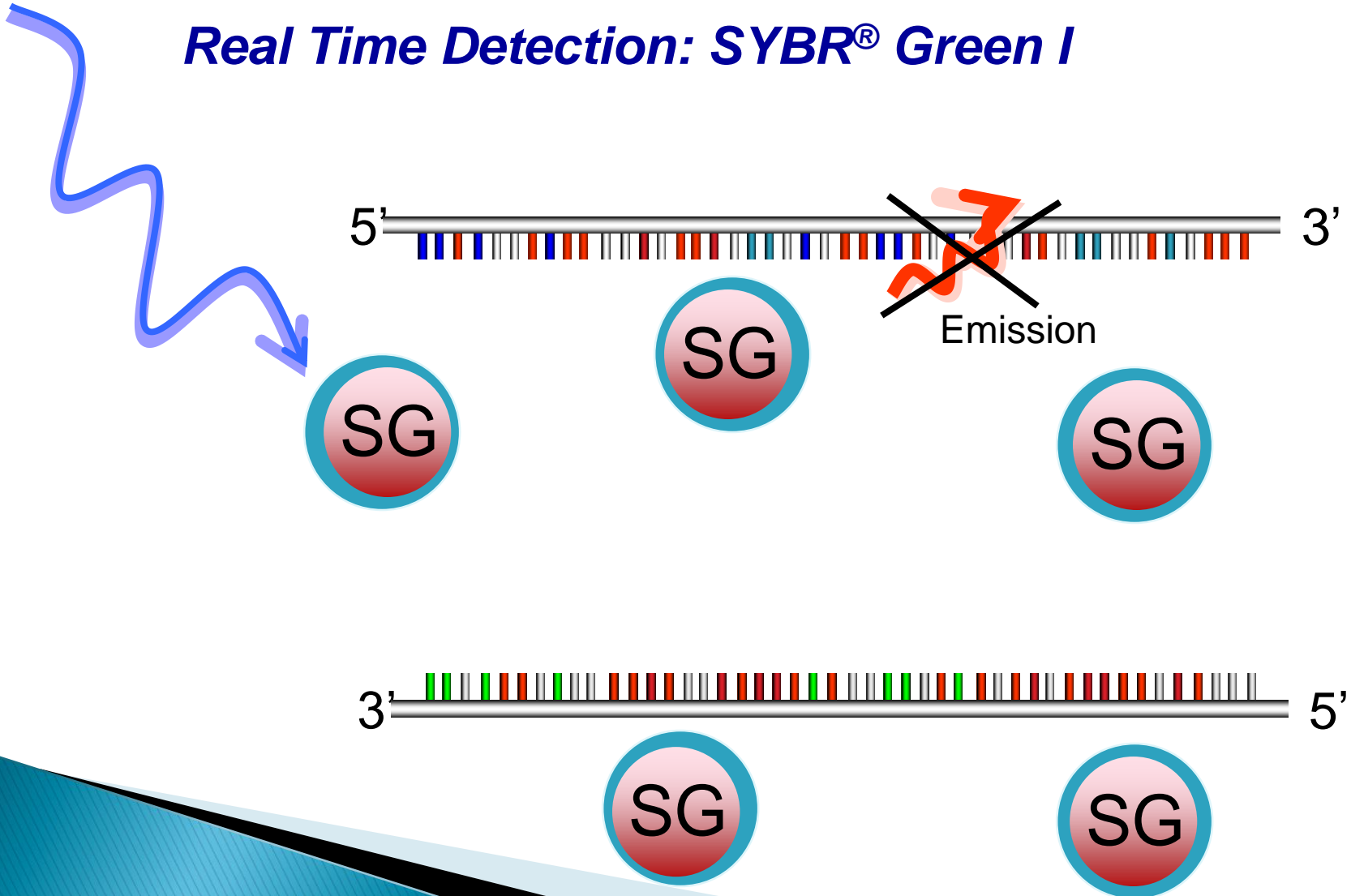


**Rn**

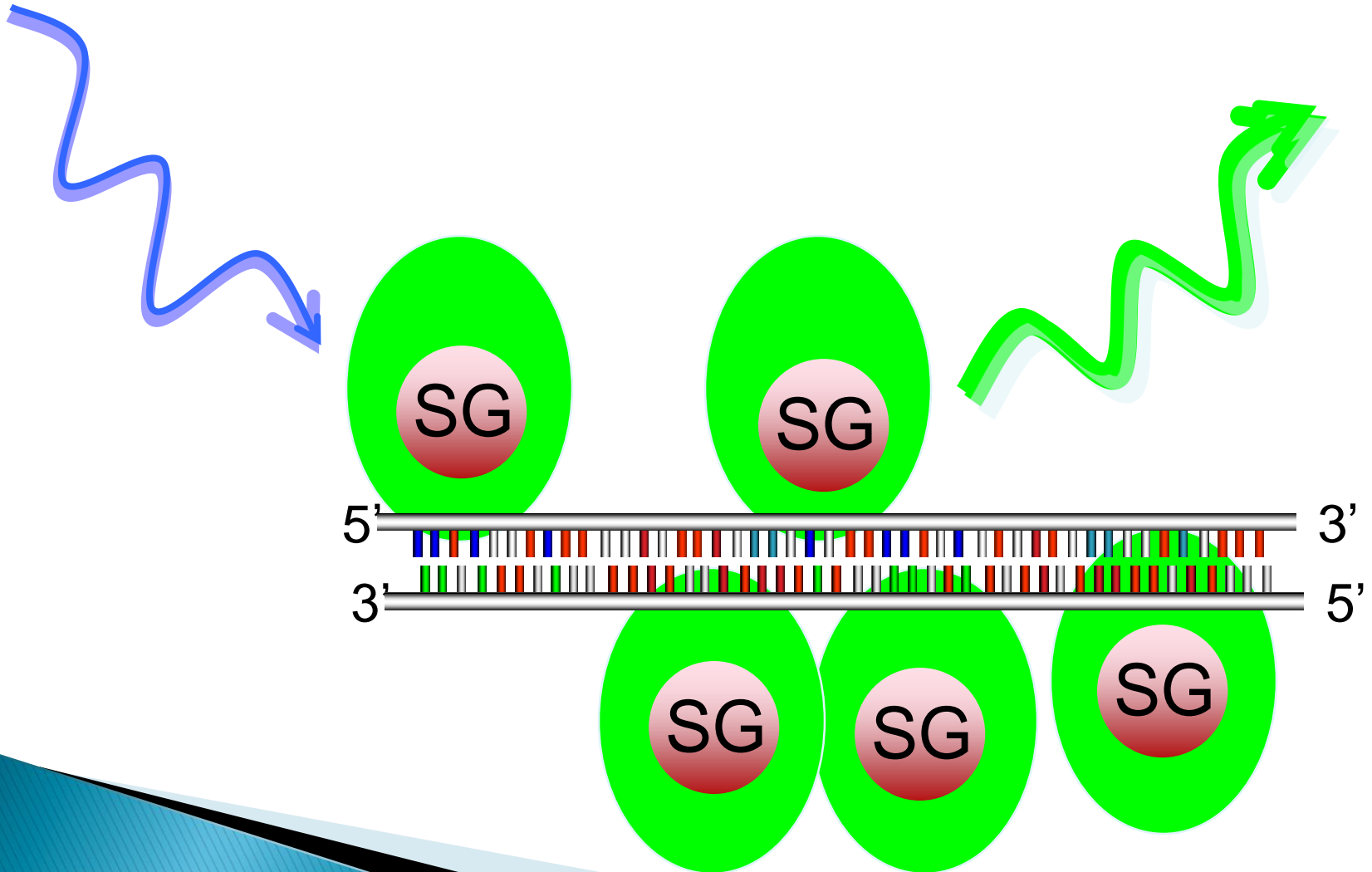




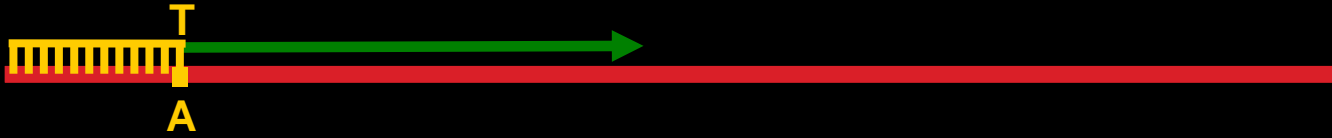
# Real Time Detection: SYBR<sup>®</sup> Green I



## Real Time Detection: SYBR<sup>®</sup> Green I



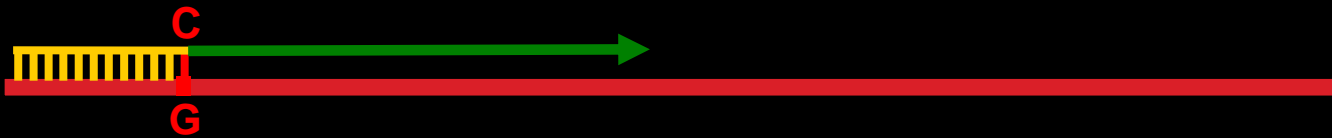
**Wt primer + Wt Sample DNA: Signal Production**



**Wt primer + Mutant Sample DNA: No Signal Production**



**Mutant primer + Mutant Sample DNA: Signal Production**



**Mutant primer + Wt Sample DNA: No Signal Production**



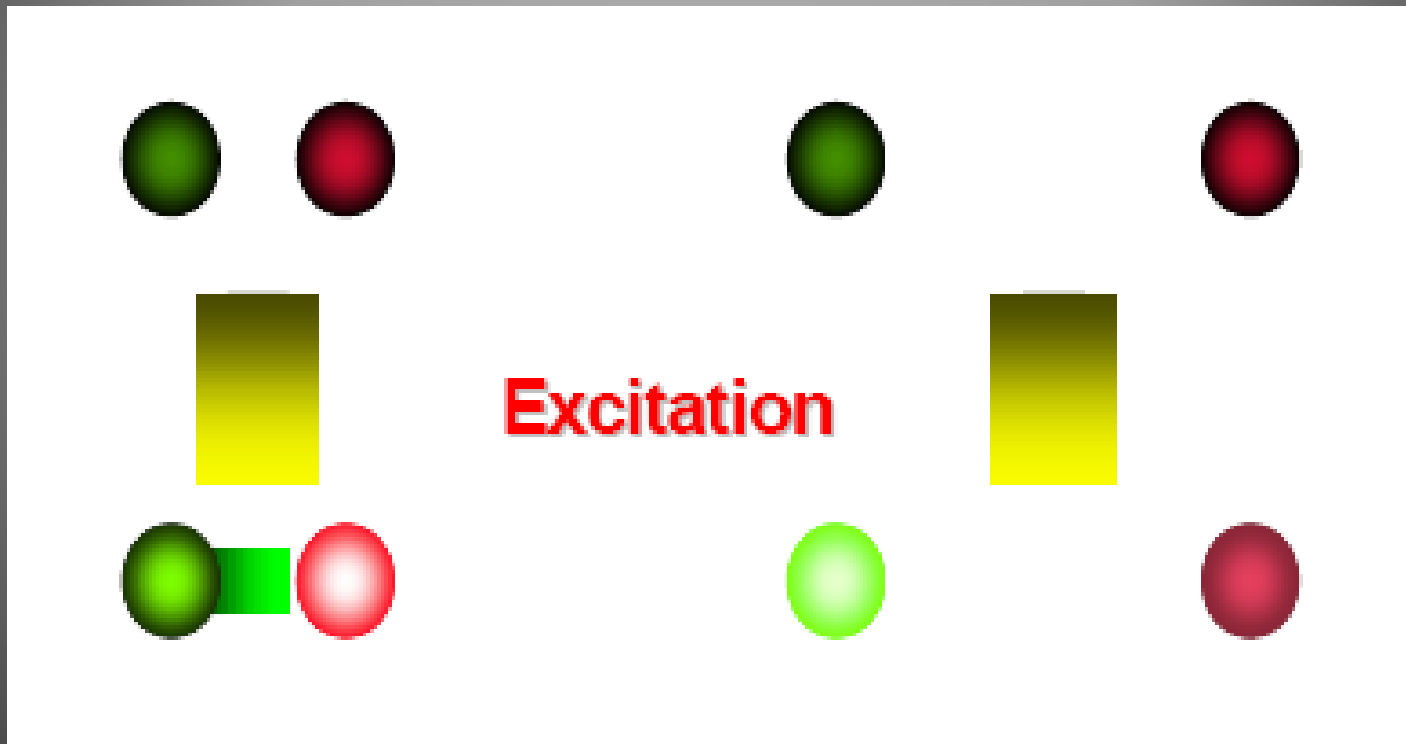
# ***Real Time Detection: SYBR® Green I***

- ▶ Positive and Negative Points
  - Easy to plan and perform
  - Cheap
  - Needs optimization
  - False signal from primer dimer and non-specific products

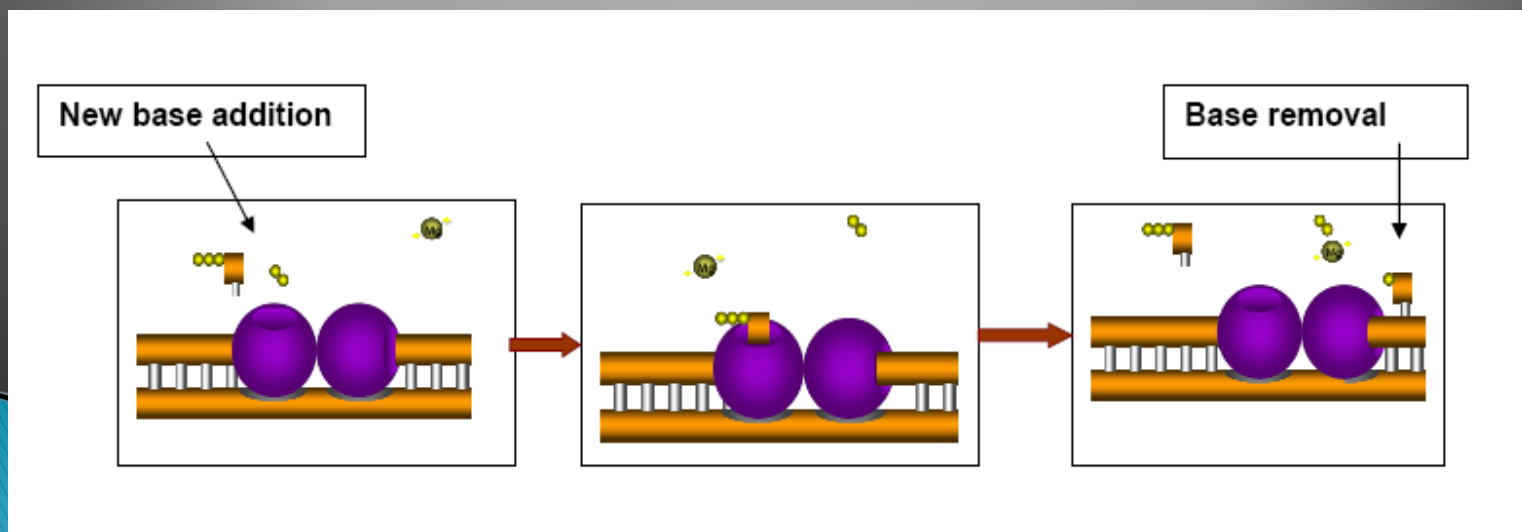
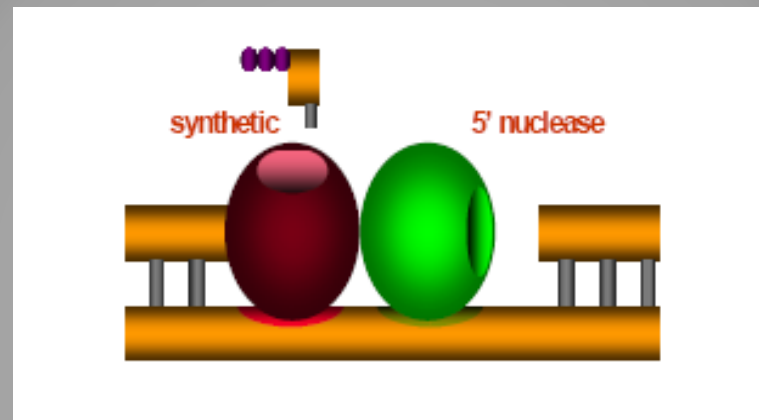
# Chemistries:

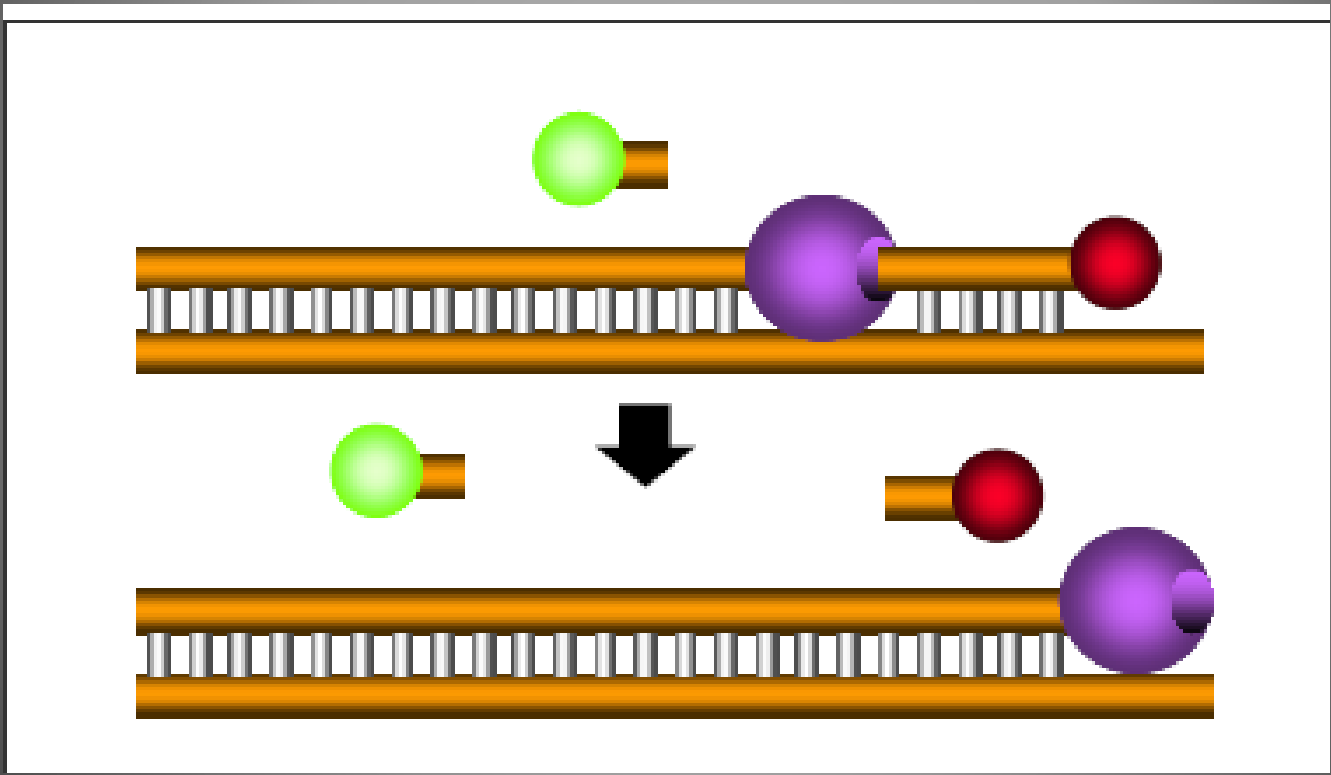
- ▶ SYBR Green
- ▶ TaqMan Probes

# FRET (Fluorescent Resonance Energy Transfer)



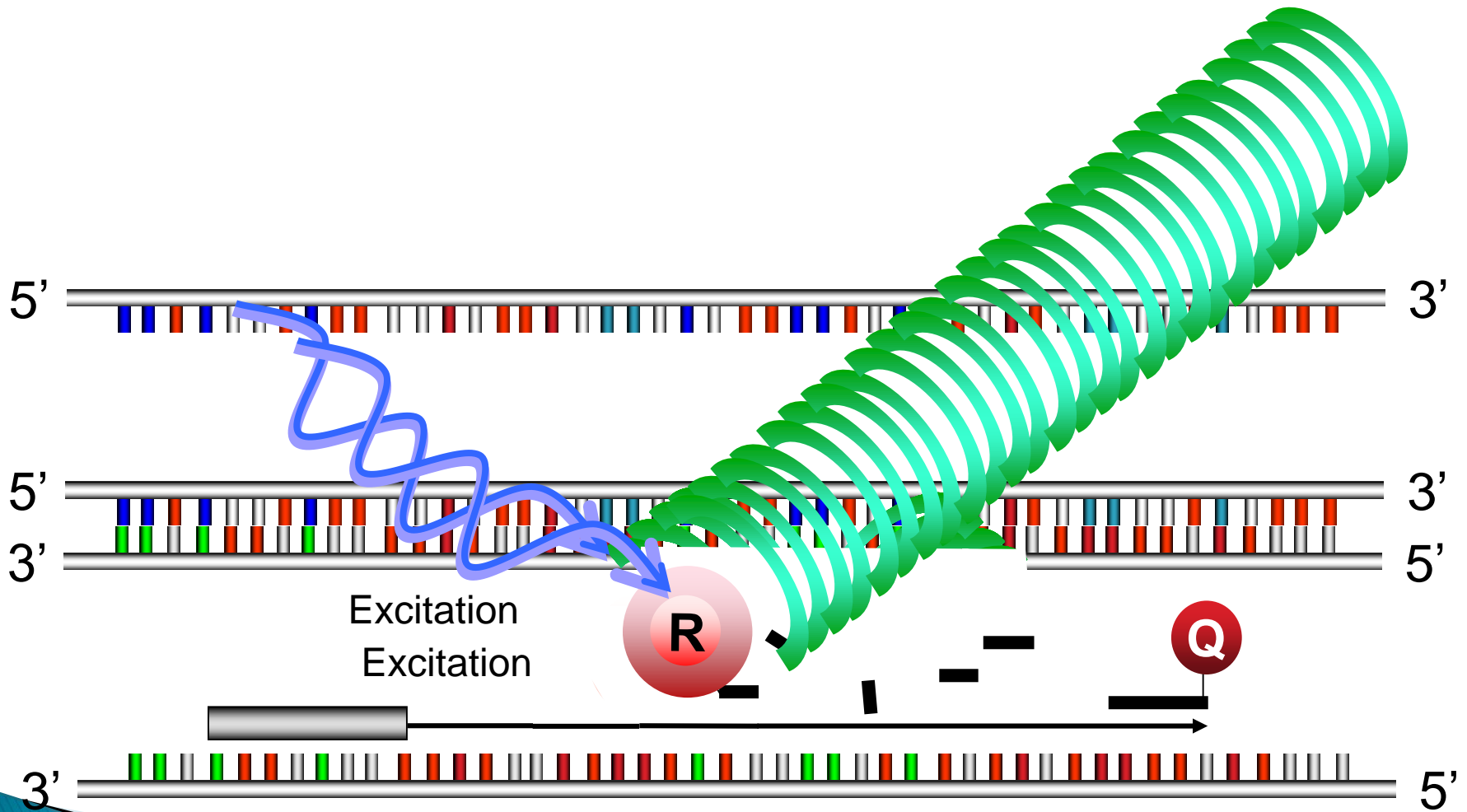
# 5' Exo-Nuclease Activity of Taq Polymerase







# Taq Man probes probes



# Primer design

## Primers

- Primers should be 20–24 bases in length.
- Short amplicons work best. Amplicon size should not exceed 300bp.
- Keep the GC content in the range of 20–80% (ideally 40–60%).
- Avoid including long sequences of identical nucleotides.
- $T_m$  should be 55 to 60°C.
- Place the forward and reverse primers as close as possible to the probe without overlapping it.

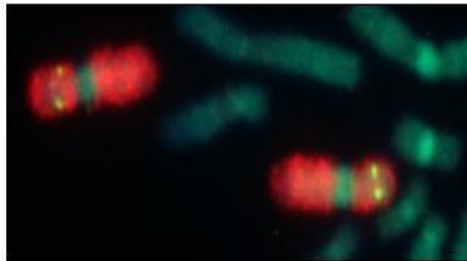
# Probe design

## Probes

- Probe should be 20–30 bases in length.
- Avoid including long sequences of identical nucleotides.
- The 5' end of a probe cannot be a guanosine residue. A guanosine residue adjacent to the reporter dye will quench some of the reporter fluorescence even after cleavage.
- The melting temperature ( $T_m$ ) of the primers should be 65 to 67°C. The probe  $T_m$  should be approximately 10°C higher than the primer  $T_m$ .
- The reporter dye should be located on the 5' end and the quencher dye should be on 3' end.

# Primer design

- ▶ If **oligo dT primers** are used in RT, the **real-time PCR primers should be picked from the 3' region** of a gene sequence to gain maximum assay sensitivity.
- ▶ If **random priming strategy** is adopted, **real-time PCR primers should be picked close to the 5' end of the target sequence** for maximum sensitivity in real-time PCR.



## Gene

Gene integrates information from a wide range of species. A record may include nomenclature, Reference Sequences (RefSeqs), maps, pathways, variations, phenotypes, and links to genome-, phenotype-, and locus-specific resources worldwide.

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[human muscular dystrophy](#)

chromosome and symbol

[\(1\[chr\] OR 2\[chr\]\) AND adh\\*\[sym\]](#)

partial name and multiple species

[alive\[prop\] AND transporter\[title\] AND \("Drosophila melanogaster"\[orgn\] OR "Mus musculus"\[orgn\]\)](#)

Home - Gene - NCBI | Rattus norvegicus follistatin | basics of primer design work | Primer 3' End Length - Google

www.ncbi.nlm.nih.gov/gene/

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- [RefSeqGene](#)
- [UniGene](#)
- [Protein Clusters](#)

### Representative queries

#### Find genes by...

#### Search text

free text

`human muscular dystrophy`

chromosome and symbol

`([chr] OR 2[chr]) AND adh*[sym]`

partial name and multiple species

`alive[prop] AND transporter[title] AND ("Drosophila melanogaster"[orgn] OR "Mus musculus"[orgn])`

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1. Fst - follistatin [Mus musculus (house mouse)]
follistatin
Official Symbol: Fst
Other Aliases: AL033346
Other Designations: FS; activin-binding protein
Location: 13
Annotation: Chromosome 13, NC\_000079.6 (114452262..114458730, complement)
ID: 14313
Order cDNA clone



2. FST - follistatin [Homo sapiens (human)]
follistatin
Official Symbol: FST
Other Aliases: FS
Other Designations: activin-binding protein; follistatin isoform FST317
Location: 5q11.2
Annotation: Chromosome 5, NC\_000005.9 (52776183..52782964)
MIM: 136470
ID: 10468
Order cDNA clone

3. Fst - follistatin [Rattus norvegicus (Norway rat)]
follistatin
Interim Symbol: Fst
Other Aliases: FOL1, Fst-288, RATFOL1
Other Designations: FS; activin-binding protein; follistatin-A
Location: 2q16
Annotation: Chromosome 2, NC\_005101.2 (65577000..65592644, complement)

- Top Organisms [Tree]
Homo sapiens (25)
Mus musculus (17)
Staphylococcus aureus subsp. aureus ST228 (8)
Staphylococcus epidermidis (3)
Sus scrofa (2)
All other taxa (126)
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## Fst follistatin [ *Rattus norvegicus* (Norway rat) ]

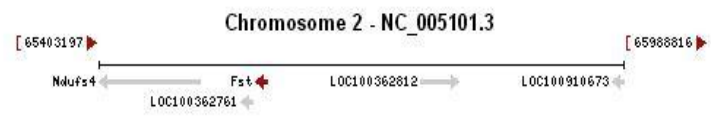
Gene ID: 24373, updated on 5-Nov-2013

### Summary ⬆ ?

- Symbol** Fst provided by RGD
- Full Name** follistatin provided by RGD
- Primary source** [RGD:2633](#)
- See related** [Ensembl:ENSRNOG00000011631](#)
- Gene type** protein coding
- RefSeq status** PROVISIONAL
- Organism** [Rattus norvegicus](#)
- Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus
- Also known as** FOL1; Fst-288; RATFOL1
- Summary** binds activin and inhibits activin-mediated signaling pathways [RGD, Feb 2006]

### Genomic context ⬆ ?

**Location:** 2q16 See Fst in [MapViewer](#)  
**Sequence:** Chromosome: 2; NC\_005101.3 (65577888..65583544, complement)



### Table of contents ⬆

- Summary
- Genomic context
- Genomic regions, transcripts, and products
- Bibliography
- Pathways
- General gene information  
Markers, Homology, Gene Ontology
- General protein information
- Reference sequences
- Related sequences
- Additional links

### Related information ⬆

- 3D structures
- BioProjects
- BioSystems
- Conserved Domains
- Full text in PMC
- Full text in PMC\_nucleotide
- Gene neighbors
- Genome



**Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus

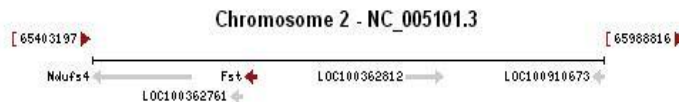
**Also known as** FOL1; Fst-288; RATFOL1

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See Fst in [MapViewer](#)



**Genomic regions, transcripts, and products**

**Genomic Sequence** NC\_005101 chromosome 2 reference Rnor\_5.0 Primary Assembly [Go to reference sequence details](#)

[Go to nucleotide](#) [Graphics](#) [FASTA](#) [GenBank](#)

Find on Sequence: [input field] [Navigation icons]

**Bibliography**

**Related articles in PubMed**

- [Proliferation of rat small hepatocytes requires follistatin expression.](#)  
Ooe H, *et al.* J Cell Physiol, 2012 Jun. PMID 21826650.
- [Structural basis for the inhibition of activin signalling by follistatin.](#)  
Harrington AE, *et al.* EMBO J, 2006 Mar 8. PMID 16482217.
- [Follistatin attenuates early liver fibrosis: effects on hepatic stellate cell activation and hepatocyte apoptosis.](#)  
Patella S, *et al.* Am J Physiol Gastrointest Liver Physiol, 2006 Jan. PMID 16123203.
- [Crystal structures of the heparan sulfate-binding domain of follistatin. Insights into ligand binding.](#)

**Additional links**

**Related information**

- 3D structures
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# Rattus norvegicus follistatin (Fst), mRNA

NCBI Reference Sequence: NM\_012561.1

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Go to:

LOCUS NM\_012561 1035 bp mRNA linear ROD 14-MAY-2013

DEFINITION Rattus norvegicus follistatin (Fst), mRNA.

ACCESSION NM\_012561

VERSION NM\_012561.1 GI:6978856

KEYWORDS RefSeq.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM [Rattus norvegicus](#)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 1035)

AUTHORS Ooe,H., Chen,Q., Kon,J., Sasaki,K., Miyoshi,H., Ichinohe,N., Tanimizu,N. and Mitaka,T.

TITLE Proliferation of rat small hepatocytes requires follistatin expression

JOURNAL J. Cell. Physiol. 227 (6), 2363-2370 (2012)

PUBMED [21826650](#)

REMARK GeneRIF: Fst expression is necessary for the proliferation of small hepatocytes.

REFERENCE 2 (bases 1 to 1035)

AUTHORS Dutra,D.B., Bueno,P.G., Silva,R.N., Nakahara,N.H., Selistre-Araujo,H.S., Nonaka,K.O. and Leal,A.M.

TITLE Expression of myostatin, myostatin receptors and follistatin in diabetic rats submitted to exercise

JOURNAL Clin. Exp. Pharmacol. Physiol. 39 (5), 417-422 (2012)

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Articles about the Fst gene

Expression of myostatin, myostatin recep [Clin Exp Pharmacol Physiol. 2012]

A potential indicator of denervated muscle atrophy: the ratio c [Genet Mol Res. 2011]

Proliferation of rat small hepatocytes requires follistatin e; [J Cell Physiol. 2012]

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Pathways for the Fst gene

Antagonism of Activin by Follistatin

Signaling by Activin

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## Rattus norvegicus follistatin (Fst), mRNA

NCBI Reference Sequence: NM\_012561.1

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```

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[Expression of myostatin, myostatin recep \[Clin Exp Pharmacol Physiol. 2012\]](#)

[A potential indicator of denervated muscle atrophy: the ratio c \[Genet Mol Res. 2011\]](#)

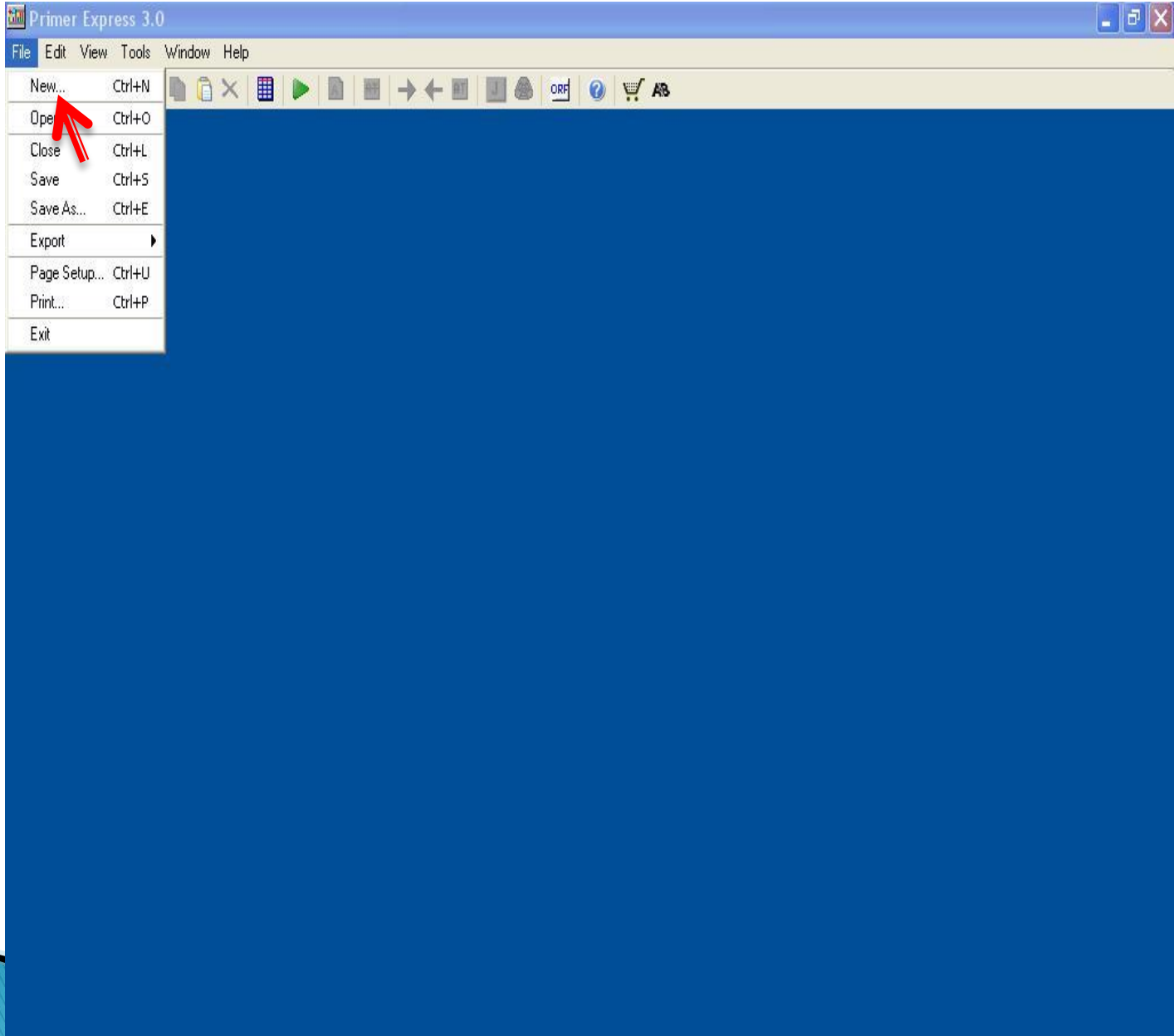
[Proliferation of rat small hepatocytes requires follistatin e \[J Cell Physiol. 2012\]](#)

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Primer Express 3.0



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Parameters:

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- TaqMan® Quantification
- TaqMan® MGB Allelic Discrimination
- TaqMan® Allelic Discrimination

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Primer Express 3.0

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TaqMan® Quantification # 2

Sequence Parameters Primers / Probes Order

File Name

Length 1035 bp. Selection 1036 to 1036  Double Stranded

ATGGTCTGCG CCAGGCACCA GCCGGGCGGG CTCTGCCTCC TGCTGTGCT 50  
 ACTCTGCCAA TTCATGGAAG ACCGCAGCGC CCAGGCTGGG AATGTGTGG 100  
 TCCGCCAAGC CAAGAACGGC CGCTGCCAGG TCCTGTATAA GACAGAACTG 150  
 AGCAAGGAAG AGTGTTCAG CACCGGCGGG CTGAGCACCT CGTGGACCGA 200  
 GGAGGATGTG AACGACAATA CTCTCTCAA GTGGATGATT TTCAACGGGG 250  
 GCGCCCCCAA CTGCATCCCT TGTAAGAAA CGTGTGAGAA TGTGGACTGT 300  
 GGCCCCGGGA AAAAGTGCCG AATGAACAAG AAGAACAAC CCCGCTGCGT 350  
 CTGTGCCCA GACTGTCCA ACATCACCTG GAAGGTCCA GTGTGTGGC 400  
 TCGATGGAA AACCTACCGC AACGAATGTG CGCTCCTCAA GGCCAGATGT 450  
 AAAAGCAGC CGGAAGTGA AGTCCAGTAC CAGGGCAAA GTAAAAAGAC 500  
 TTGCAGGGAT GTTTTCTGTC CAGGCAGTCC CACTTGTGTG GTGGATCAGA 550  
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 CTGCCACCTG AGAAAAGCCA CCTGCTTGCT GGGCAGATCC ATTGGATTAG 700  
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 CTCTCTCTGC GATGAGCTGT GCCCGACAG TAAGTCGGAT GAGCCCGTCT 850  
 GTGCCACCGA CAATGCCACG TACGCCAGCG AGTGTGCCAT GAAGGAAGCT 900  
 GCCTGCTCCT CCGGCGTACT GCTTGAAGTG AAGCACTCCG GATCTTGCAA 950  
 CTCCATCTCG GAAGAAACGG AGGAAGAGGA GGAAGAGGAA GACCAGGACT 1000  
 ACAGCTTCCC TATCTCTTCC ACTCTAGAGT GGTAA 1035

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TaqMan® Quantification # 2

Sequence Parameters Primers / Probes Order

File Name FST

Length 1035 bp. Selection 351 to 351  Double Stranded



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AGCAAGGAAG AGTGTTCAG CACCGGCCG	200
GGAGGATGTG AACGACAATA CTCTTTCA	250
GCGCCCCCAA CTGCATCCCT TGTAAAGAA	300
GGCCCCGGGA AAAAGTGCCT AATGAACAA	350
CTGTGCCCA GACTGTCCA ACATCACCT	400
TCCATGGGAA AACCTACGC AACGAATGT	450
AAAGAGCAGC CGGAACCTGA AGTCCAGTA	500
TTGCAGGGAT GTTTCTGTC CAGGCAGCT	550
CCAATAATGC CTAAGTGTG ACCTGTAAT	600
TCTTCAGAGC AGTCCCTTTG CCGGAACGA	650
CTGCCACCTG AGAAAGGCCA CCTGCTTGC	700
CCTATGAGGG AAAAGTATC AAAGCAAAG	750
GGTGGTGGAA AAAAATGCCT ATGGGATTT	800
CTCTCTCTGC GATGAGCTGT GCCCGGACA	850
GTGCCAGCGA CAATGCCACG TACGCCAGC	900
GCCTGCTCCT CCGGCCTACT GCTTGAAGT	950
CTCCATCTCG GAAGAACGG AGGAAGAGG	1000
ACAGCTTCCC TATCTCTCC ACTCTAGAG	1035

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File name:

Files of type: Primer Express 3.0 Document (.pxd)

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TaqMan® Quantification # 2

Sequence Parameters Primers / Probes Order

File Name: FST

Length: 1035 bp. Selection: 401 to 401  Double Stranded

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ATGGTCTGCG CCAGGCACCA GCCCGCGGG CTCTGCCTCC TGCTGCTGCT 50
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GGAGGATGTG AACGACAATA CTCTCTTCAA GTGGATGATT TTCAACGGGG 250
GCGCCCCCAA CTGCATCCCT TGTAAGAAAA CGTGTGAGAA TGTGGACTGT 300
GGCCCCGGGA AAAAGTGCCG AATGAACAAG AAGAACAAC CCCGCTGCGT 350
CTGTGCCCCA GACTGTTCCA ACATCACCTG GAAGGGTCCA GTGTGTGGGC 400
TCGATGGGAA AACCTACCGC AACGAATGTG CGCTCCTCAA GGCCAGATGT 450
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CCAATAATGC CTACTGTGTG ACCTGTAATC GGATTTGCCG GGAACCTCA 600
TCTTCAGAGC AGTCCCTTTG CGGAACGAT GGTGTGACTT ACTCCAGTGC 650
CTGCCACCTG AGAAAAGCCA CCTGCTTGCT GGGCAGATCC ATTGGATTAG 700
CCTATGAGGG AAAGTGTATC AAAGCAAAGT CTTGTGAAGA CATCCAGTGC 750
GGTGGTGAA AAAAATGCCT ATGGGATTTT AAGGTTGGCA GAGTCCGCTG 800
CTCTCTCTGC GATGAGCTGT GCCCGGACAG TAAGTCGGAT GAGCCCGTCT 850
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CTCCATCTCG GAAGAAACGG AGGAAGAGGA GGAAGAGGAA GACCAGGACT 1000
ACAGCTTCCC TATCTCTTCC ACTCTAGAGT GGTA 1035
```





Sequence Parameters Primers / Probes Order

Candidate Primers & Probes

#	Fwd Start	Fwd Len...	Fwd Tm	Fwd %GC	Rev Start	Rev Len...	Rev Tm	Rev %GC	Probe Start	Probe Le...	Probe Tm	Probe %GC	An
1	47	22	59	45	106	17	59	65	71	18	69	78	85
2	47	22	59	45	107	16	58	63	71	18	69	78	84
3	47	22	59	45	108	17	60	59	71	18	69	78	84
4	47	22	59	45	108	16	60	63	71	18	69	78	84
5	44	21	58	48	106	17	59	65	68	19	69	74	85
6	44	21	58	48	106	17	59	65	68	20	69	70	85
7	44	21	58	48	106	17	59	65	69	19	68	74	85
8	44	21	58	48	106	17	59	65	71	18	69	78	85
9	44	22	59	45	106	17	59	65	68	19	69	74	85
10	44	22	59	45	106	17	59	65	68	20	69	70	85
11	44	22	59	45	106	17	59	65	71	18	69	78	85
12	45	22	59	50	107	16	58	63	68	19	69	74	85
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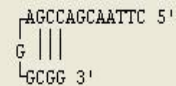
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Secondary Structure

Oligo	Length
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<input checked="" type="radio"/> Reverse Primer	17
<input type="radio"/> Probe	18
Forward Primer	
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Reverse Primer	
GGCGGAGCCAGCAATTC	
Probe	
ACCGCAGCGCCAGGCTG	

Hairpin Self Dimers Cross Dimers

Most Stable Structure Found





TaqMan® Quantification # 2

Sequence Parameters Primers / Probes Order

Candidate Primers & Probes

#	Fwd Start	Fwd Len...	Fwd Tm	Fwd %GC	Rev Start	Rev Len...	Rev Tm	Rev %GC	Probe Start	Probe Le...	Probe Tm	Probe %GC	An
1	47	22	59	45	106	17	59	65	71	18	69	78	85
2	47	22	59	45	107	16	58	63	71	18	69	78	84
3	47	22	59	45	108	17	60	59	71	18	69	78	84
4	47	22	59	45	108	16	60	63	71	18	69	78	84
5	44	21	58	48	106	17	59	65	68	19	69	74	85
6	44	21	58	48	106	17	59	65	68	20	69	70	85
7	44	21	58	48	106	17	59	65	69	19	68	74	85
8	44	21	58	48	106	17	59	65	71	18	69	78	85
9	44	22	59	45	106	17	59	65	68	19	69	74	85
10	44	22	59	45	106	17	59	65	68	20	69	70	85
11	44	22	59	45	106	17	59	65	71	18	69	78	85
12	45	22	59	50	107	16	58	63	68	19	69	74	85
13	45	22	59	50	107	16	58	63	68	20	69	70	85
14	45	22	59	50	107	16	58	63	69	19	68	74	85

Location



Secondary Structure

Oligo	Length
<input checked="" type="radio"/> <b>Forward Primer</b>	21
<input type="radio"/> Reverse Primer	17
<input type="radio"/> Probe	20

Forward Primer  
TGCTGCTACTCTGCCAATTCA

Reverse Primer  
GGCGGAGCCAGCAATTC

Probe  
AAGACCGCAGCGCCAGGCT

Hairpin
Self Dimers
Cross Dimers

Most Stable Structure Found

Hairpins not found



## TaqMan® Quantification # 2

Sequence Parameters Primers / Probes Order

Parameter	Value
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Max Primer Tm	60
Max Difference in Tm of Two Primers	2
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Max Primer %GC Content	80
Max Primer 3' GC's	2
Primer 3' End Length	5
Primer 3' GC Clamp Residues	0
<input type="checkbox"/> Primer Length	
Min Primer Length	9
Max Primer Length	40
Optimal Primer Length	20
<input type="checkbox"/> Primer Composition	
Max Primer G Repeats	3
Max Num Ambig Residues in Primer	0
<input type="checkbox"/> Primer Secondary Structure	
Max Primer Consec Base Pair	4
Max Primer Total Base Pair	8
<input type="checkbox"/> Primer Site Uniqueness	
Max % Match in Primer	75
Max Consec Match in Primer	9
Max 3' Consec Match in Primer	7
<input type="checkbox"/> Probe Tm	
Min Probe Tm	68
Max Probe Tm	70
<input type="checkbox"/> Probe GC Content	
Min Probe %GC Content	30
Max Probe %GC Content	80
<input type="checkbox"/> Probe Length	
Min Probe Length	13
Max Probe Length	30

Factory Defaults

Primer Express 3.0

File Edit View Tools Window Help

TaqMan® Quantification # 2

Sequence Parameters Primers / Probes Order

Parameter	Value
Max Primer G Repeats	3
Max Num Ambig Residues in Primer	0
<input type="checkbox"/> Primer Secondary Structure	
Max Primer Consec Base Pair	4
Max Primer Total Base Pair	8
<input type="checkbox"/> Primer Site Uniqueness	
Max % Match in Primer	75
Max Consec Match in Primer	9
Max 3' Consec Match in Primer	7
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Min Probe Tm	68
Max Probe Tm	70
<input type="checkbox"/> Probe GC Content	
Min Probe %GC Content	30
Max Probe %GC Content	80
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Min Probe Length	13
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Max Num Ambig Residues in Probe	0
No G at 5' End in Probe	<input checked="" type="checkbox"/>
Select Probe with more C's than G's	<input checked="" type="checkbox"/>
<input type="checkbox"/> Probe Secondary Structure	
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Max Probe Total Base Pair	8
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Factory Defaults

Primer Express 3.0

File Edit View Tools Window Help

TaqMan® Quantification # 2

Sequence Parameters Primers / Probes Order

File Name: FST

Length: 1035 bp. Selection: 401 to 401  Double Stranded

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GCCTGCTCCT	CCGGCGTACT	GCTTGAAGTG	AAGCACTCCG	GATCTTGCAA	950
CTCCATCTCG	GAAGAAACGG	AGGAAGAGGA	GGAAAGAGAA	GACCAGGACT	1000
ACAGCTTCCC	TATCTCTTCC	ACTCTAGAGT	GGTAA		1035

Gene Gene adiponectin homo sapiense

Search

Save search Limits Advanced

Help

Display Settings: Summary, 20 per page, Sorted by Relevance

Send to:

Filter your results:

You are currently running Internet Explorer 7, which is not supported by NCBI web applications. More information

Showing results for adiponectin homo sapiens. Search instead for adiponectin homo sapiense (0)

- All (194)
- Current Only (192)
- Genes Genomes (187)
- SNP GeneView (184)
- In Variation Viewer (99)

Manage Filters

Results: 1 to 20 of 194

<< First < Prev Page 1 of 10 Next > Last >>

ADIPOQ - adiponectin, C1Q and collagen domain containing [Homo sapiens]

1. adiponectin, C1Q and collagen domain containing

Official Symbol: ADIPOQ

Other Aliases: ACDC, ACRP30, ADIPQTL1, ADPN, APM-1, APM1, GBP28

Other Designations: 30 kDa adipocyte complement-related protein; adipocyte complement-related 30 kDa protein; adiponectin; adipose most abundant gene transcript 1 protein; adipose specific collagen-like factor; gelatin-binding protein 28

Location: 3q27

Annotation: Chromosome 3, NC\_000003.11 (186560463..186576252)

MIM: 605441

ID: 9370

Order cDNA clone

Find related data

Database: Select

Find items

CDH13 - cadherin 13, H-cadherin (heart) [Homo sapiens]

2. cadherin 13, H-cadherin (heart)

Official Symbol: CDH13

Other Aliases: CDHH, P105

Search details

adiponectin[All Fields] AND ("Homo sapiens"[Organism] OR homo sapiens[...])

Gene Gene [input field]

Search

Limits Advanced

Help

Display Settings: Full Report

Send to:

# ADIPOQ adiponectin, C1Q and collagen domain containing [ *Homo sapiens* ]

Gene ID: 9370, updated on 17-Feb-2013

## Summary

**Official Symbol** ADIPOQ provided by HGNC

**Official Full Name** adiponectin, C1Q and collagen domain containing provided by HGNC

**Primary source** [HGNC:13633](#)

**See related** [Ensembl:ENSG00000181092](#); [HPRD:05671](#); [MIM:605441](#); [Vega:OTTHUMG00000156521](#)

**Gene type** protein coding

**RefSeq status** REVIEWED

**Organism** [Homo sapiens](#)

**Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo

**Also known as** ACDC; ADPN; APM1; APM-1; GBP28; ACRP30; ADIPQTL1

**Summary** This gene is expressed in adipose tissue exclusively. It encodes a protein with similarity to collagens X and VIII and complement factor C1q. The encoded protein circulates in the plasma and is involved with metabolic and hormonal processes. Mutations in this gene are associated with adiponectin deficiency. Multiple alternatively spliced variants, encoding the same protein, have been identified. [provided by RefSeq, Apr 2010]

## Table of contents

- Summary
- Genomic context
- Genomic regions, transcripts, and products
- Bibliography
- Phenotypes
- HIV-1 protein interactions
- Interactions
- General gene info
- General protein info
- Reference sequences
- Related sequences
- Additional links

## Related information

- Order cDNA clone

30 kDa adipocyte complement-related protein  
 adipocyte complement-related 30 kDa protein  
 adipose most abundant gene transcript 1 protein

▲ NCBI Reference Sequences (RefSeq)
 ⌵ ?

☐ [RefSeqs maintained independently of Annotated Genomes](#)

These reference sequences exist independently of genome builds. [Explain](#)

**Genomic**

1.	<b>NG_021140.1 RefSeqGene</b>	
	Range	5001..20790
	Download	<a href="#">GenBank</a> , <a href="#">FASTA</a> , <a href="#">Sequence Viewer (Graphics)</a>

**mRNA and Protein(s)**

1.	<b><a href="#">NM_001177800.1</a> → <a href="#">NP_001171271.1</a> adiponectin precursor</b>	
	Status:	REVIEWED
	Description	Transcript Variant: This variant (1) represents the longer transcript. Both variants 1 and 2 encode the same protein.
	Source sequence(s)	<a href="#">AC072018</a> , <a href="#">AC112907</a> , <a href="#">AK312868</a>
	Consensus CDS	<a href="#">CCDS3284.1</a>
	UniProtKB/TrEMBL	<a href="#">A8K660</a>
	UniProtKB/TrEMBL	<a href="#">B2R773</a>



Nucleotide

Nucleotide

Search

Limits Advanced

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Send:

# Homo sapiens adiponectin, C1Q and collagen domain containing (ADIPOQ), transcript variant 1, mRNA

NCBI Reference Sequence: NM\_001177800.1

[FASTA](#) [Graphics](#)

Go to:

LOCUS NM\_001177800 4629 bp mRNA linear PRI 17-FEB-2013

DEFINITION Homo sapiens adiponectin, C1Q and collagen domain containing (ADIPOQ), transcript variant 1, mRNA.

ACCESSION NM\_001177800

VERSION NM\_001177800.1 GI:295317371

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM [Homo sapiens](#)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4629)

Change region shown

Customize view

### Analyze this sequence

- Run BLAST
- Pick Primers
- Highlight Sequence Features
- Find in this Sequence

### Articles about the ADIPOQ gene

Adiponectin and long-term mortality in ... cor [Arterioscler Thromb Vasc Biol. 20...

666-870

AK312868.1

636-840

871-4629

AC072018.6

7231-10989

FEATURES

source

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Recent activity

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Homo sapiens adiponectin, C1Q and collagen domain containing Nucleot

Homo sapiens anti-Mullerian hormone (AMH), RefSeqGene Nucleot

AMH anti-Mullerian hormone [Homo sapiens] Ge

amh homo sapiens (15)

Homo sapiens adiponectin, C1Q and collagen domain containing Nucleot

See mor

polyA signal

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GBP28"

polyA site

4629

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GBP28"

ORIGIN

5'

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Nucleotide

Nucleotide [dropdown] [input field]

Search

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Send:

# Homo sapiens adiponectin, C1Q and collagen domain containing (ADIPOQ), transcript variant 1, mRNA

NCBI Reference Sequence: NM\_001177800.1

[FASTA](#) [Graphics](#)

Go to:

LOCUS NM\_001177800 4629 bp mRNA linear PRI 17-FEB-2013

DEFINITION Homo sapiens adiponectin, C1Q and collagen domain containing (ADIPOQ), transcript variant 1, mRNA.

ACCESSION NM\_001177800

VERSION NM\_001177800.1 GI:295317371

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM [Homo sapiens](#)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4629)

Change region shown

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Pick Primers

Highlight Sequence Features

Find in this Sequence

Articles about the ADIPOQ gene

Adiponectin and long-term mortality in cor [Arterioscler Thromb Vasc Biol. 2013]

[Display Settings:](#)  FASTA

[Send:](#)

# Homo sapiens adiponectin, C1Q and collagen domain containing (ADIPOQ), transcript variant 1, mRNA

NCBI Reference Sequence: NM\_001177800.1

[GenBank](#) [Graphics](#)

>gi|295317371|ref|NM\_001177800.1| Homo sapiens adiponectin, C1Q and collagen domain containing (ADIPOQ), transcript variant 1, mRNA

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Change region shown

Customize view

Analyze this sequence

[Run BLAST](#)

[Pick Primers](#)

[Highlight Sequence Features](#)

[Find in this Sequence](#)

Articles about the ADIPOQ gene

[Adiponectin and long-term mortality in cor \[Arterioscler Thromb Vasc Biol. 2013\]](#)

[Genetic association of adiponectin with type 2 diabetes in Jordanian \[Gene. 2013\]](#)

[Effects of omega-3 fatty acids supplementa \[Asia Pac J Clin Nutr. 2012\]](#)

[See all...](#)

**Design at least one primer and/or  
*probe* which crosses one *exon*  
*junction***